

Sequence alignment of protein 1lhow_Ymr21 across various species. The alignment shows sequence conservation and divergence. A color scale at the top indicates sequence identity: red for identical, green for conservative substitutions, blue for semi-conservative substitutions, and purple for non-conservative substitutions. The x-axis represents amino acid positions from 10 to 190. The y-axis lists protein accessions for each species.

Color Legend:

- Red: Identical
- Green: Conservative Substitution
- Blue: Semi-Conservative Substitution
- Purple: Non-Conservative Substitution

Accessions (Y-axis):

- 15238114.p
- 15238314.p
- AK073808.q
- AK103469.q
- 83563413.q
- AK064909.q
- 61270024.q
- 15229881.p
- 15221868.p
- 15241289.p
- 47490017.q
- 15219169.p
- AK072696.q
- 83513309.q
- AK068916.q
- 83590929.q
- MAMASSLAAANHPLPSKPLSCIKPLTRATPLSRLAHAGAAAAARGASSSQEELRPPDSKNAPALSAELRLARVGRDPSALALLDILSHRGVPATASAFALLTACRSLAHARQVHAHLRVHGLDSNEFLILLARIVELYLAIGAREDARKVLGDLRASSFSWNALLHHGVRRGRQGAAVVDCFAEMRAAGADANEY
- 15217565.p
- 15223647.p
- 30681286.p
- 15217643.p
- 15217521.p
- 15241455.p
- 15218897.p
- 15235867.p
- 46580004.q
- 15221833.p
- 15221219.p
- AK067238.q
- 22330784.p
- 22327464.p
- 83593689.q
- 83511868.q
- 1fvv_CDk2
- 1cm8_P38g
- 1jwh_CK2a
- 1lhow_Ymr21

Position Labels (X-axis):

- 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190
- 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390

	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990		
1000																				
15238114.p	MAMASFGQLN	I	EEPPPIGSRVDF	CPEKLEQ																	
15238314.p	MAAAFGQLN	I	EEPPPIGSRVDF	CPEKLEQ																	
AK073808.q	MAVAAPGQLN	L	DESP-SVG-SVDF	CPEKLEQ																	
AKL03469.q	MAVAAPGQLN	L	DESP-SVG-SVDF	CPEKLEQ																	
83563413.q	MDGEEAPPGQLN	L	ADY-A-PAGARTV	CDRERK																	
AK064909.q	APAAAEE	O	LAAP-TP-LVVA	VAGEALRVT	P-RAD	T-PFKLNK															
61270024.q	N-KARCE	O	VAAA-TP-PALVAA	VAGDAID	T-PERAD	SPEKIDK															
15229881.p	KNLLOGE	O	VAAA-TPS-LSE	VCGEALS-C	LEKAD	SPEKIDK															
15221868.p	K-HWGR	O	VAAA-TPS-LSD	ACGEALN	A-VPEKAD	T-PFKLNK															
15241289.p	-R-GMSL	R	TYPE-TP-LIA	ACGDS-IKDIT	TP-RAD	VPEKLNK															
47490017.q	-RAVEGE	O	VAAA-TP-LVS	VAAEAVR	VPEKLNK	SPEKIDK															
15219169.p	-KATEGE	O	YVAAC-TP-LAS	VAGEAIVR	VPEKLNK	SPEKIDK															
AK072696.p	VPNGVQGG	H	ATP-LVPT-LTE	VAAEAVR	VPEKLNK	SPEKIDK															
83513309.q	VPQFQSE	H	TAAC-TPS-LTS	VAGEAIVR	VPEKLNK	SPEKIDK															
AK068916.q	K-OFPSE	H	BNTVMPD-LMK	Vapeavoc	OFPR-RAD	SPEKIDK															
83590929.q	ELKGLS	H	VAAA-TPS-LAS	VAGEAIVN	VPEKLNK	SPEKIDK															
15217565.p	VSNDRGA	K	VAAA-TPS-LVS	VAGEAIVN	VPEKLNK	SPEKIDK															
15223647.p	VSNDRAA	K	VAAA-TPS-LVS	VAGEAIVN	VPEKLNK	SPEKIDK															
30681286.p	15217643.p	VPRSAEAE	L	AA-TP-LTS	VAGEAIK	VPEKLNK	SPEKIDK														
15217521.p	RVISNKTE	R	AA-TP-LPS-LAS	VAGEAIK	VPEKLNK	SPEKIDK															
15241455.p	VVIDPSPETVSKRAE	L	AA-TP-LPS-LAS	VAGEAIK	VPEKLNK	SPEKIDK															
15218897.p	IVSPKDAE	R	KQ-VAA-TP-LVS	VAGEAI	VLPV-FRAN	I-PFKLNK															
46580004.q	VHFRSS	L	AA-TP-LSS	AA-GDALA	VAPR-SAD	A-PFKLNK															
15221833.p	-YLEAE	O	VAA-TP-LSN	VAGEAI	H-VWPFR	SD	A-PFKLNK														
15221219.p	-YLEAE	O	VAA-TP-LSN	VAGEAI	H-VWPFR	SD	A-PFKLNK														
AK067238.p	SLECE	O	VAA-TP-LSA	VAGEAI	Q-WIP-LKAD	SPEKIDK															
22330784.p	NVEAE	O	VAAA-TP-LSS	AA-PEAVH-VWPFR	AE-DPE	TP-EK															
22327464.p	QAAAE	O	AA-TP-LALCS	AA-PEAVH-VWPFR	AE-DPE	TP-EK															
83593689.q	PPTR	S	STT-QARTV	TE-HLSF-SIKLT	LLINGT	GGS-MTO															
83511868.q	TPAPAPQAPR	R	DE	ED	DP	TL	LDNV	REALQ	SIV	PSAD	ANDK-TAK	ARTCTAMP	PPW	ASLATL	ITAKTESL	MAAA	MDGCCW	SVYKA			
1fvv_CDk2	1cm8_P38g	MEN	F	POKE	V	TEC	EV	FL	EV	FL	EV	FL	EV	FL	EV	FL	EV	FL	EV		
1jwh_CK2a	MSGPVPSR	SGFYR	EV	VKT	A	WE	RAV	YR	DOP	V	EG	V	CF	YR	PSR	T	ALV	EHN	N		
1how_Ymr21	DYRP	GGFHP	A	FK	CEP	YK	NDAR	Y	IL	Y	IL	Y	IL	Y	ND	ADNT	KEDSMG	ANHIL	LDHF	NKGPNG	
1200																				
15238114.p	LRFT	V	QIKCYM	ROLLT	T	LEH	CHVNQ	V	VLHRDIK	G	SNLIL	DNC	N	N	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
15238314.p	LRFT	V	QIKCYM	ROLLT	T	LEH	CHVNQ	V	VLHRDIK	G	SNLIL	DNC	N	N	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
AK073808.q	MRFT	V	QIKCYM	ROLLT	T	LEH	CHVNQ	V	VLHRDIK	G	SNLIL	DNC	N	N	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
AKL03469.q	MRFT	V	QIKCYM	ROLLT	T	LEH	CHVNQ	V	VLHRDIK	G	SNLIL	DNC	N	N	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
83563413.q	-T	P	QVK	YQ	ML	K	LG	YH	CHVNQ	V	VLHRDIK	DYLPFF	IG	LL	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
AK064909.q	-DVKF	P	QVK	YQ	ML	K	LG	YH	CHVNQ	V	VLHRDIK	DYLPFF	IG	LL	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
61270024.q	-EIKFT	P	QVK	YQ	ML	K	LG	YH	CHVNQ	V	VLHRDIK	DYLPFF	IG	LL	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
15229881.p	-EIKFT	P	QVK	YQ	ML	K	LG	YH	CHVNQ	V	VLHRDIK	DYLPFF	IG	LL	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
15221868.p	VVKFS	E	EVK	C	DR	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL
15241289.p	-CLKFD	L	QVK	CF	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
47490017.q	-QVKFD	L	QVK	CF	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
15219169.p	-AIFKFS	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
AK072696.q	-CIKFT	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
83513309.q	-CIRFT	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
AK068916.q	-CIKFT	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
83590929.q	-CLIKFS	E	QOIK	CF	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
15217565.p	-CINFS	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
15223647.p	-IKFS	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
30681286.p	-IKFS	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
15217521.p	-IKFS	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
15241455.p	-IKFS	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
15218897.p	-CVFKS	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
15235867.p	-CVFKS	E	QVK	CY	ML	Q	LL	CH	HS	RG	V	HL	DI	KLAD	GLAR	S	SH	DHTGN	TNRV	ITL	
46580004.q	-ADCP	A	DP	QPL	QHAY	G	NRN	L	EQ	R	PL	QH	Y	DL	Q	PS	SH	EQ	Q	PL	PS
15221833.p	-DIFT	A	DP	QPL	QHAY	G	NRN	L	EQ	R	PL	QH	Y	DL	Q	PS	SH	EQ	Q	PL	PS
15221219.p	-DIFT	A	DP	QPL	QHAY	G	NRN	L	EQ	R	PL	QH	Y	DL	Q	PS	SH	EQ	Q	PL	PS
AK067238.p	-DIFT	A	DP	QPL	QHAY	G	NRN	L	EQ	R	PL	QH	Y	DL	Q	PS	SH	EQ	Q	PL	PS
22330784.p	-DIFT	A	DP	QPL	QHAY	G	NRN	L	EQ	R	PL	QH	Y	DL	Q	PS	SH	EQ	Q	PL	PS
22327464.p	-DIFT	A	DP	QPL	QHAY	G	NRN	L	EQ	R	PL	QH	Y	DL	Q	PS	SH	EQ	Q	PL	PS
83593689.q	-DIFS	A	DP	QPL	QHAY	G	NRN	L	EQ	R	PL	QH	Y	DL	Q	PS	SH	EQ	Q	PL	PS
83511868.q	KMLATW	E	GGG	ADE	VKR	KRL	ST	KA	IN	RAV	GR	SGS	WFA	R	GT	PR	KY	CM	Y	GT	PR
1fvv_CDk2	A-IG	I	PL	PL	IG	Y	LE	Q	LL	CH	HS	RG	V	HL	DI	PL	IG	Y	GT	PR	
1cm8_P38g	YD	I	PL	PL	IG	Y	LE	Q	LL	CH	HS	RG	V	HL	DI	PL	IG	Y	GT	PR	
1how_Ymr21	CIP	I	LY	VI	QI	SK	LL	CH	HS	RG	V	HL	DI	PL	IG	Y	GT	PR			

